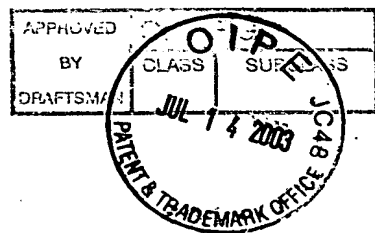


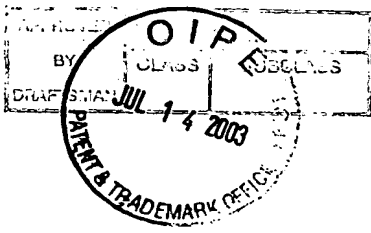
Title: 125P5C8: A TISSUE SPECIFIC PROTEIN HIGHLY  
EXPRESSED IN VARIOUS CANCERS  
First Inventor: Mary FARIS  
Application No.: 09/809,638  
Docket No.: 511582003500



1/10

GATCACGTGCTGTCGATATCCTTCACATTGCCATGTTTCAGTGAGCTGTAGATAATCTCT  
GGAGCCAGGTGCTGAAGTGATATATCCCAGAAATATCACTTGATTAGAGCTACTTTTCA  
GTAGTTTTTGAACAGCAATAGCCTGCAGTTTCCTGTCGAGGTCATCTTCGTGGTTCCCA  
AAGTGTGTCACGACAAAATCCACCAGCTTGCCCGAAATGTTAACGGTCAATGTGATGGC  
TGGTGCGATCTTGCTGTGTTGGCCAGGCTGGTCTCAACGTGCAGATAGATC

Figure 1



Title: 125P5C8: A TISSUE SPECIFIC PROTEIN HIGHLY  
EXPRESSED IN VARIOUS CANCERS  
First Invented by: Mary FARIS  
Application No.: 09/809,638  
Docket No.: 511582003500

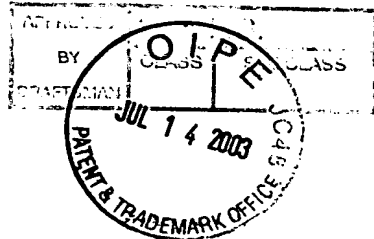
2/10

```

      M   T   S   L   W   R   E   I   L   L   E   S   L   L   G   C   V   S
1    ATG ACC TCG CTG TGG AGA GAA ATC CTC TTG GAG TCG CTG CTG GGA TGT GTT TCT
      W   S   L   Y   H   D   L   G   P   M   I   Y   Y   F   P   L   Q   T
55   TGG TCT CTC TAC CAT GAC CTG GGA CCG ATG ATC TAT TAC TTT CCT TTG CAA ACA
      L   E   L   T   G   L   E   G   F   S   I   A   F   L   S   P   I   F
109  CTA GAA CTC ACT GGG CTT GAA GGT TTT AGT ATA GCA TTT CTT TCT CCA ATA TTC
      L   T   I   T   P   F   W   K   L   V   N   K   K   W   M   L   T   L
163  CTA ACA ATT ACT CCT TTC TGG AAA TTG GTT AAC AAG AAG TGG ATG CTA ACC CTG
      L   R   I   I   T   I   G   S   I   A   S   F   Q   A   P   N   A   K
217  CTG AGG ATA ATC ACT ATT GGC AGC ATA GCC TCC TTC CAG GCT CCA AAT GCC AAA
      L   R   L   M   V   L   A   L   G   V   S   S   L   I   V   Q   A
271  CTT CGA CTG ATG GTT CTT GCG CTT GGG GTG TCT TCC TCA CTG ATA GTG CAA GCT
      V   T   W   W   S   G   S   H   L   Q   R   Y   L   R   I   W   G   F
325  GTG ACT TGG TGG TCG GGA AGT CAT TTG CAA AGG TAC CTC AGA ATT TGG GGA TTC
      I   L   G   Q   I   V   L   V   V   L   R   I   W   Y   T   S   L   N
379  ATT TTA GGA CAG ATT GTT CTT GTT GTT CTA CGC ATA TGG TAT ACT TCA CTA AAC
      P   I   W   S   Y   Q   M   S   N   K   V   I   L   T   L   S   A   I
433  CCA ATC TGG AGT TAT CAG ATG TCC AAC AAA GTG ATA CTG ACA TTA AGT GCC ATA
      A   T   L   D   R   I   G   T   D   G   D   C   S   K   P   E   E   K
487  GCC ACA CTT GAT CGT ATT GGC ACA GAT GGT GAC TGC AGT AAA CCT GAA GAA AAG
      K   T   G   E   V   A   T   G   M   A   S   R   P   N   W   L   L   A
541  AAG ACT GGT GAG GTA GCC ACG GGG ATG GCC TCT AGA CCC AAC TGG CTG CTG GCA
      G   A   A   F   G   S   L   V   F   L   T   H   W   V   F   G   E   V
595  GGG GCT GCT TTT GGT AGC CTT GTG TTC CTC ACC CAC TGG GTT TTT GGA GAA GTC
      S   L   V   S   R   W   A   V   S   G   H   P   H   P   G   P   D   P
649  TCT CTT GTT TCC AGA TGG GCA GTG AGT GGG CAT CCA CAT CCA GGG CCA GAT CCT
      N   P   F   G   G   A   V   L   L   C   L   A   S   G   L   M   L   P
703  AAC CCA TTT GGA GGT GCA GTA CTG CTG TGC TTG GCA AGT GGA TTG ATG CTT CCA
      S   C   L   W   F   R   G   T   G   L   I   W   W   V   T   G   T   A
757  TCT TGT TTG TGG TTT CGT GGT ACT GGT TTG ATC TGG TGG GTT ACA GGA ACA GCT
      S   A   A   G   L   L   Y   L   H   T   W   A   A   A   V   S   G   C
811  TCA GCT GCG GGG CTC CTT TAC CTG CAC ACA TGG GCA GCT GCT GTG TCT GGC TGT
      V   F   A   I   F   T   A   S   M   W   P   Q   T   L   G   H   L   I
865  GTC TTC GCC ATC TTT ACT GCA TCC ATG TGG CCC CAA ACA CTT GGA CAC CTT ATT
      N   S   G   T   N   P   G   K   T   M   T   I   A   M   I   F   Y   L
919  AAC TCA GGG ACA AAC CCT GGG AAA ACC ATG ACC ATT GCC ATG ATA TTT TAT CTT
      L   E   I   F   F   C   A   W   C   T   A   F   K   F   V   P   G   G
973  CTA GAA ATA TTT TTC TGT GCC TGG TGC ACA GCT TTT AAG TTT GTC CCA GGA GGT
      V   Y   A   R   E   R   S   D   V   L   L   G   T   M   M   L   I   I
1027 GTC TAC GCT AGA GAA AGA TCA GAT GTG CTT TTG GGG ACA ATG ATG TTA ATT ATC
      G   L   N   M   L   F   G   P   K   K   N   L   D   L   L   L   Q   T
1081 GGG CTG AAT ATG CTA TTT GGT CCT AAG AAA AAC CTT GAC TTG CTT CTT CAA ACA
      K   N   S   S   K   V   L   F   R   K   S   E   K   Y   M   K   L   F
1135 AAA AAC AGT TCT AAA GTG CTT TTC AGA AAG AGT GAA AAA TAC ATG AAA CTT TTT
      L   W   L   L   V   G   V   G   L   L   G   L   G   L   R   H   K   A
1189 CTG TGG CTG CTT GTT GGT GTG GGA TTG TTG GGA TTA GGA CTA CGG CAT AAA GCC
      Y   E   R   K   L   G   K   V   A   P   T   K   E   V   S   A   A   I
1243 TAT GAG AGA AAA CTG GGC AAA GTG GCA CCA ACC AAA GAG GTC TCT GCT GCC ATC
      W   P   F   R   F   G   Y   D   N   E   G   W   S   S   L   E   R   S
1297 TGG CCT TTC AGG TTT GGA TAT GAC AAT GAA GGG TGG TCT AGT CTA GAA AGA TCA
      A   H   L   L   N   E   T   G   A   D   F   I   T   I   L   E   S   D
1351 GCT CAC CTG CTC AAT GAA ACA GGT GCA GAT TTC ATA ACA ATT TTG GAG AGT GAT
      A   S   K   P   Y   M   G   N   N   D   L   T   M   W   L   G   E   K

```

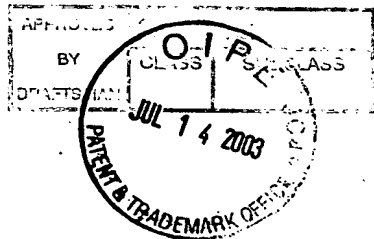
Figure 2A



3/10

1405 GCT TCT AAG CCC TAT ATG GGG AAC AAT GAC TTA ACC ATG TGG CTA GGG GAA AAG  
L G F Y T D F G P S T R Y H T W G I  
1459 TTG GGT TTC TAT ACA GAC TTT GGT CCA AGC ACA AGG TAT CAC ACT TGG GGG ATT  
M A L S R Y P I V K S E H H L L P S  
1513 ATG GCT TTG TCA AGA TAC CCA ATT GTG AAA TCT GAG CAT CAC CTT CTT CCG TCA  
P E G E I A P A I T L T V N I S G K  
1567 CCA GAG GGC GAG ATC GCA CCA GCC ATC ACA TTG ACC GTT AAC ATT TCG GGC AAG  
L V D F V V T H F G N H E D D L D R  
1621 CTG GTG GAT TTT GTC GTG ACA CAC TTT GGG AAC CAC GAA GAT GAC CTC GAC AGG  
K L Q A I A V S K L L K S S S N Q V  
1675 AAA CTG CAG GCT ATT GCT GTT TCA AAA CTA CTG AAA AGT AGC TCT AAT CAA GTG  
I F L G Y I T S A P G S R D Y L Q L  
1729 ATA TTT CTG GGA TAT ATC ACT TCA GCA CCT GGC TCC AGA GAT TAT CTA CAG CTC  
T E H G N V K D I D S T D H D R W C  
1783 ACT GAA CAT GGC AAT GTG AAG GAT ATC GAC AGC ACT GAT CAT GAC AGA TGG TGT  
E Y I M Y R G L I R L G Y A R I S H  
1837 GAA TAC ATT ATG TAT CGA GGG CTG ATC AGG TTG GGT TAT GCA AGA ATC TCC CAT  
A E L S D S E I Q M A K F R I P D D  
1891 GCT GAA CTG AGT GAT TCA GAA ATT CAG ATG GCA AAA TTT AGG ATC CCT GAT GAC  
P T N Y R D N Q K V V I D H R E V S  
1945 CCC ACT AAT TAT AGA GAC AAC CAG AAA GTG GTC ATA GAC CAC AGA GAA GTT TCT  
E K I H F N P R F G S Y K E G H N Y  
1999 GAG AAA ATT CAT TTT AAT CCC AGA TTT GGA TCC TAC AAA GAA GGA CAC AAT TAT  
E N N H H F H M N T P K Y F L \*  
2053 GAA AAC AAC CAT CAT TTT CAT ATG AAT ACT CCC AAA TAC TTT TTA TGA AAC

Figure 2B

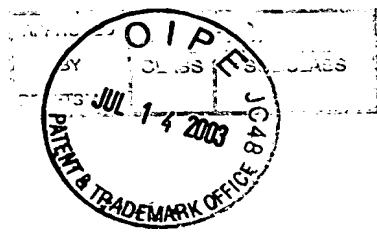


Title: 125P5C8: A TISSUE SPECIFIC PROTEIN HIGHLY  
EXPRESSED IN VARIOUS CANCERS  
First Inventor: Mary FARIS  
Application No.: 09/809,638  
Docket No.: 511582003500

4/10

1	MTSLWREILL	ESLLGCVSWS	LYHDLGPMIY	YFPLQTLELT	GLEGFSIAFL	50
51	SPIFLTITPF	WKLVNKKWML	TLLRIITIGS	IASFQAPNAK	LRLMVLALGV	100
101	SSSLIVQAVT	WWSGSHLQRY	LRIWGFILGQ	IVLVVLRIWY	TSLNPIWSYQ	150
151	MSNKVILTLS	AIATLDRIGT	DGDCSKPEEK	KTGEVATGMA	SRPNWLLAGA	200
201	AFGSLVFLTH	WVFGEVSLVS	RWAVSGHPHP	GPDPNPFGGA	VLLCLASGLM	250
251	LPSCWLFRGT	GLIWWVTGTA	SAAGLLYLHT	WAAAVSGCVF	AIFTASMWPQ	300
301	TLGHLINSGT	NPGKMTMIAM	IFYLLEIFFC	AWCTAFKFVP	GGVYARERSD	350
351	VLLGTMMMLII	GLNMLFGPKK	NLDLLLQTKN	SSKVLFRKSE	KYMKLFLWLL	400
401	VGVGLLGLGL	RHKAYERKLG	KVAPTKEVSA	AIWPFREFGYD	NEGWSSLERS	450
451	AHLLNETGAD	FITILES DAS	KPYMGNNDLT	MWLGEKLGFY	TDFGPSTRYH	500
501	TWGIMALSRY	PIVKSEHHLL	PSPEGEIAPA	ITLTVNISGK	LVDFVVTHFG	550
551	NHEDDLDRKL	QAIHAVSKLLK	SSSNQVIFLG	YITSAPGSRD	YLQLTEHGNV	600
601	KDIDSTDHDR	WCEYIMYRGL	IRLGARISH	AELSDSEIQM	AKFRIPDDPT	650
651	NYRDNQKVI	DHREVSEKIH	FNPRFGSYKE	GHNYENNHHF	HMNTPKYFL	699

Figure 3



5/10

Score = 1397 bits (3615), Expect = 0.0  
Identities = 682/699 (97%), Positives = 683/699 (97%)

Query: 1 MTS LWREILLES LLGCVSWSLY HDLGPMIYYFPLQTLELTGLEGFSIAFLSPIFLTITPF 60  
MTSLWREILLES LLGCVSWSLY HDLGPMIYYFPLQTLELTGLEGFSIAFLSPIFLTITPF  
Sbjct: 1 MTS LWREILLES LLGCVSWSLY HDLGPMIYYFPLQTLELTGLEGFSIAFLSPIFLTITPF 60

Query: 61 WKL VNKKWMLTLLRIITIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGSHLQRY 120  
WKL VNKKWMLTLLRIITIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGSHLQRY  
Sbjct: 61 WKL VNKKWMLTLLRIITIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGSHLQRY 120

Query: 121 LRIWGFILGQIVLVVLRIWYTS LNPIWSYQMSNKVILTLSAIATLD RIGTDGDCSKPEEK 180  
LRIWGFILGQIVLVVLRIWYTS LNPIWSYQMSNKVILTLSAIATLD RIGTDGDCSKPEEK  
Sbjct: 121 LRIWGFILGQIVLVVLRIWYTS LNPIWSYQMSNKVILTLSAIATLD RIGTDGDCSKPEEK 180

Query: 181 KTGEVATGMASRPNWLLAGAAFGSLVFLTHWVFGEVSLVSRWAVSGHPHPGDPNPF GGA 240  
KTGEVATGMASRPNWLLAGAAFGSLVFLTHWVFGEVSLVSRWAVSGHPHPGDPNPF GGA  
Sbjct: 181 KTGEVATGMASRPNWLLAGAAFGSLVFLTHWVFGEVSLVSRWAVSGHPHPGDPNPF GGA 240

Query: 241 VLLCLASGLMLPSC LWFRGTGLIWWVTGTASAAGLLYLHTWAAAVSGCVFAIFTASMWPQ 300  
VLLCLASGLMLPSC LWFRGTGLIWWVTGTASAAGLLYLHTWAAAVSGCVFAIFTASMWPQ  
Sbjct: 241 VLLCLASGLMLPSC LWFRGTGLIWWVTGTASAAGLLYLHTWAAAVSGCVFAIFTASMWPQ 300

Query: 301 TLGHLINSGTNPGKMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSDVLLGTMM LII 360  
TLGHLINSGTNPGKMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSDVLLGTMM LII  
Sbjct: 301 TLGHLINSGTNPGKMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSDVLLGTMM LII 360

Query: 361 GLNMLFGPKKNLDLL LQTKNSSKVLFRKSEKYM KXXXXXXXXXXXXXXXXX RHKAYERKLG 420  
GLNMLFGPKKNLDLL LQTKNSSKVLFRKSEKYM RHKAYERKLG  
Sbjct: 361 GLNMLFGPKKNLDLL LQTKNSSKVLFRKSEKYM KFLWLLVGVGLLGLRHKAYERKLG 420

Query: 421 KVAPTKEVSAAIWPFRFGYDNEGWS SLERSAHLNETGADFITILES DASKPYMGNNDLT 480  
KVAPTKEVSAAIWPFRFGYDNEGWS SLERSAHLNETGADFITILES DASKPYMGNNDLT  
Sbjct: 421 KVAPTKEVSAAIWPFRFGYDNEGWS SLERSAHLNETGADFITILES DASKPYMGNNDLT 480

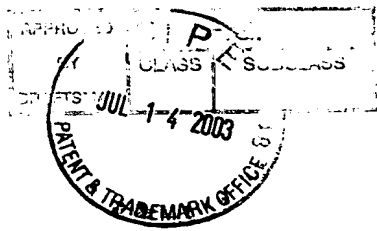
Query: 481 MWLGEKLG FYTDFGPSTRYHTWGIMALSRYPIVKSEHLLPSPEGEIAPAITLT VNISGK 540  
MWLGEKLG FYTDFGPSTRYHTWGIMALSRYPIVKSEHLLPSPEGEIAPAITLT VNISGK  
Sbjct: 481 MWLGEKLG FYTDFGPSTRYHTWGIMALSRYPIVKSEHLLPSPEGEIAPAITLT VNISGK 540

Query: 541 LVDFVVT HFGNHEDDLDRKLQAI AVSKLLKSSSNQVIFLGYITSAPGSRDY LQLTEHGNV 600  
LVDFVVT HFGNHEDDLDRKLQAI AVSKLLKSSSNQVIFLGYITSAPGSRDY LQLTEHGNV  
Sbjct: 541 LVDFVVT HFGNHEDDLDRKLQAI AVSKLLKSSSNQVIFLGYITSAPGSRDY LQLTEHGNV 600

Query: 601 KDIDSTDHDRWCEYIMYRGLIRLGYARISHAELSDSEIQMAKFRI PDDPTNYRDNQKVVI 660  
KDIDSTDHDRWCEYIMYRGLIRLGYARISHAELSDSEIQMAKFRI PDDPTNYRDNQKVVI  
Sbjct: 601 KDIDSTDHDRWCEYIMYRGLIRLGYARISHAELSDSEIQMAKFRI PDDPTNYRDNQKVVI 660

Query: 661 DHREVSEKIHFNPRFGSYKEGHNYENNNH FHMNTPKYFL 699  
DHREVSEKIHFNPRFGSYKEGHNYENNNH FHMNTPKYFL  
Sbjct: 661 DHREVSEKIHFNPRFGSYKEGHNYENNNH FHMNTPKYFL 699

Figure 4A



6/10

Score = 261 bits (668), Expect = 1e-68  
Identities = 204/705 (28%), Positives = 330/705 (45%), Gaps = 50/705 (7%)

Query: 15 GCVSWSLYHDLGPMIYYFPLQTLTLELTGLEGFSAFLSPIFLTITPFWKLVNKKWMLTLLR 74  
G + WS L I++FPL + ++G E + +L PIFL + PF ++ + L  
Sbjct: 279 GFLFWSNVTSLLCSIWHFPLWYMGISGYEAAILGYLGPIFLYL-PFVSEAFQTQYGVLLGG 337

Query: 75 IITIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGSHLQ-RYLRIWGFILGQIVL 133  
II IG+ Q P +L + + ++ + VQ + + + + + W +LG +  
Sbjct: 338 IIAIGAYI-VQMPELRLISVAVGTSITVATFVQNLRYITNAETSFSFALTW--LLGLVAS 394

Query: 134 VVLRIWYTSLNPIWSYQMS-----NKVILTLSAIATLDRIGTDGDCSKPEEKKTGEVATG 188  
V+L++ + + NP W NK L L+ + + + + E K+ + +  
Sbjct: 395 VILKMGFYTNPTWVILDERNGGYNKTALVLTVLFGM--LSPYVNSINFEGKRNAQAKS- 451

Query: 189 MASRPNWLLAGAAFGSLVFLTHWVFEVSLVSRWAVSGHHPH-GPDNPFGGAVLLCLAS 247  
AS L FGSL+F H + + S WA G+ GP P P+G L C  
Sbjct: 452 -ASLIGKLFLAVGFGSLLFGIHLQLLTDSSTTIYWAWEGYNESHGFLPWPWGA--LTCTVM 508

Query: 248 GLMLPSCWFRGTGLIWWVTGTASAAGLLY--LHTWAAAV-SGCVFAIFTASMWPQ---T 301  
S + F G L+ + S A L + W + G ++AI + P  
Sbjct: 509 LFASLSSVKFMGKPLVPCLLLLISTAVLSARSITQWPKYIFGGLLYAIAMWLVP SYFSA 568

Query: 302 LGHLINSGTNPCKTMTIAMIFYLLEIFFCAWCTAFKFPVGGVYARERSDVLLGTMMLIIG 361  
LG + N ++ Y++ + W A+ FVP G RE+ + +L I  
Sbjct: 569 LGQVQNIWV-----YVLSFSVYIIFVLAHVWVVAYAFVPMGWVLRKIETVLAFSSTFII 623

Query: 362 LNMLFGPKKNLDLLLQTKNSSKVLFRKSEKYMKXXXXXXXXXXXXXXXXXXXXRHKAYERKLK 421  
+ L N+ L+ K +F R R G  
Sbjct: 624 IGALTCKNLNIQLVTMGKKFFIYVF-----FFAVALLSLTARFVYDIRPTGI 670

Query: 422 VAP-----TKEVSAAIWPFREFGYDNEGWSLERSAHLNETGADFITILES DASKPYMGNN 477  
P ++ ++A IW FG DN+ W+S +R +L+ + D + +LE+D + MGN  
Sbjct: 671 PQPYHPDSQLITAGIWTIHFGLDNDMWASEDRMINLIKDMELDVVGLLETDQTRITMGNR 730

Query: 478 DLTMWLGEKLGFTYDFGPSTRYHTWGIMALSRYPIVKSEHLLPSPEGEIAPAITLTV-N 536  
DLT L L Y DFGP HTWG + LS++PIV S HHLLPSP GE+APAI T+  
Sbjct: 731 DLTSLAHDNLNMYADFGPGPNKHTWGCVLLSKFPIVNSTHLLPSPVGELAPAIHATLQT 790

Query: 537 ISGKLVDFVVTHTFGNHEDDLDRKLQAIIVSKLLKSSSNQVIFLGYITSAPGSRDY-LQLT 595  
+ LVD V H G ED+ DR+LQ+ ++KL+ +++ I L Y+ PG +Y ++  
Sbjct: 791 YNDTLVDVVFVHSGQEEDRRLQSNYMAKLMGNTRPAILLSYLVVDPGEGNYNTYVS 850

Query: 596 EHGNVKDIDSTDHWRCEYIMYRGLRLGYARISHAELSDSEIQMAKFRIPDDPTNYRDN 655  
E + DID +D DRWCEYI+YRGL R GYAR++ ++D+E+Q+ KF++ + ++  
Sbjct: 851 ETSGMHDIDPSDDRWCEYIYRGLRRTGYARVARGTITDTLQVGVKFQVLSEQA-LVEH 909

Query: 656 QKVVIDHREVSEKIHFNPRFGSYKEGHNYENNHFFHM-NTPKYFL 699  
+ ++ +SE + + +F G E H +H+ + P+Y+L  
Sbjct: 910 SDSMYEYGHMSEPEYEDMKFPDKFLGEG-ERGHFYHVFDEPRYYL 953

Figure 4B

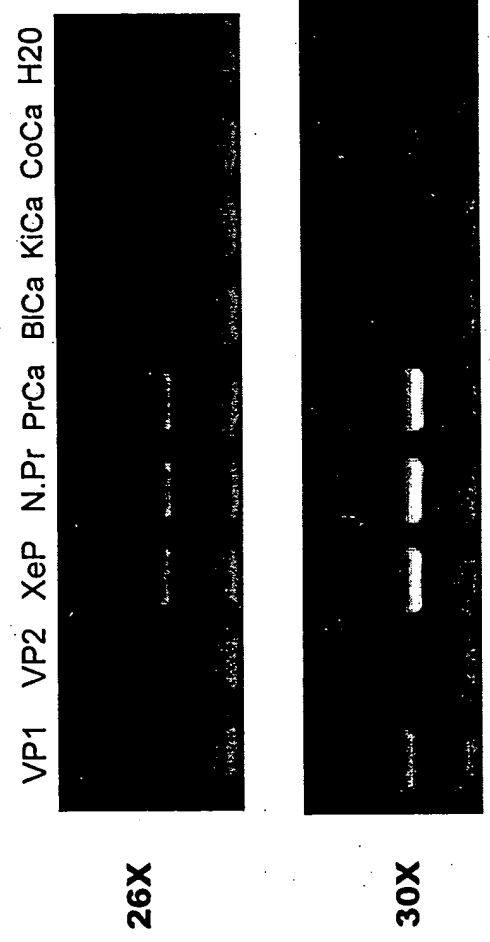
18379 U.S. PTO  
07/14/03

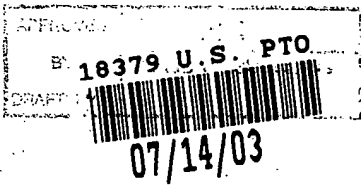
Title: 125P5C8: A TISSUE SPECIFIC PROTEIN HIGHLY  
EXPRESS IN VARIOUS CANCERS  
First Inventor: Mary FARIS  
Application No.: 09/809,638  
Docket No.: 511582003500

7/10

BEST AVAILABLE COPY

Figure 5





Title: 125P5C8: A TISSUE SPECIFIC PROTEIN HIGHLY  
EXPRESSED IN VARIOUS CANCERS  
First Inventor: Mary FARIS  
Application No.: 09/809,638  
Docket No.: 511582003500

BEST AVAILABLE COPY

8/10

Figure 6C

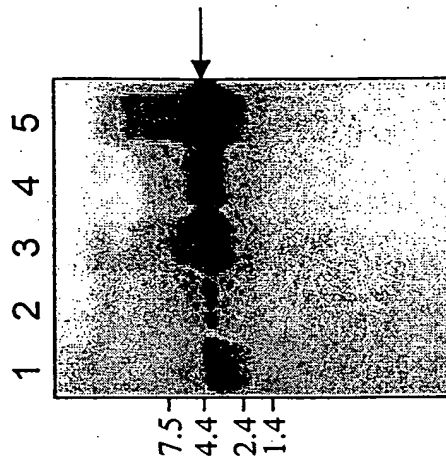


Figure 6B

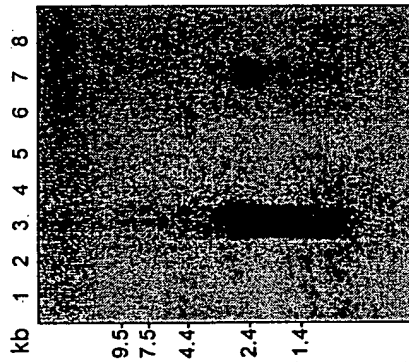
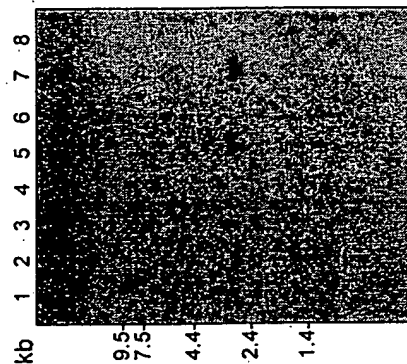


Figure 6A





18379 U.S. PTO



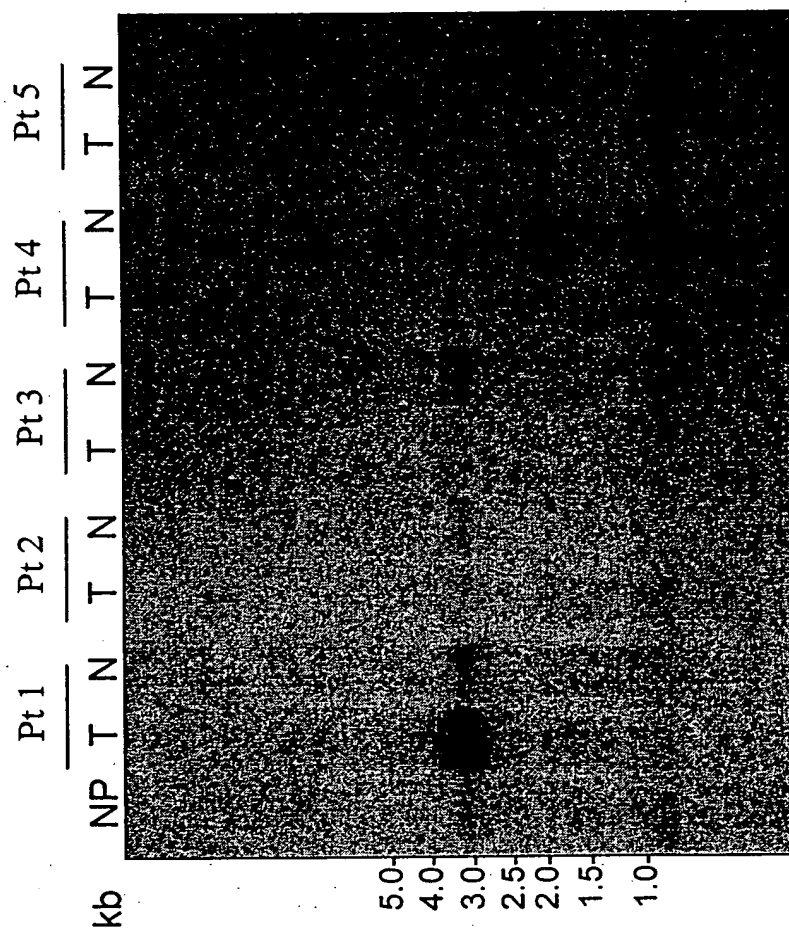
07/14/03

EXPRESSED IN VARIOUS CANCERS  
First Inve: Mary FARIS  
Application No.: 09/809,638  
Docket No.: 511582003500

9/10

BEST AVAILABLE COPY

Figure 7



18379 U.S. PTO  
07/14/03

Title: 125P5C8: A TISSUE SPECIFIC PROTEIN HIGHLY  
EXPRESSED IN VARIOUS CANCERS  
First Inventor: Mary FARIS  
Application No.: 09/809,638  
Docket No.: 511582003500

BEST AVAILABLE COPY

10/10

Figure 8

